



## SEQUENCE LISTING

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Mrsny, Randall J.  
The Government of the United States of America  
as represented by The Secretary of the  
Department of Health and Human Services  
Genentech, Inc.

<120> Pseudomonas Exotoxin A-Like Chimeric Immunogens for  
Eliciting a Secretory IgA-Mediated Immune Response

<130> 015280-361200US

<140> US 10/659,036

<141> 2003-09-09

<150> US 60/056,924

<151> 1997-07-11

<150> WO PCT/US98/14336

<151> 1998-07-10

<150> US 09/462,713

<151> 2000-05-12

<160> 13

<170> PatentIn Ver. 2.1

<210> 1

<211> 1839

<212> DNA

<213> Pseudomonas aeruginosa

<220>

<221> CDS

<222> (1)..(1839)

<223> exotoxin A

<400> 1

gcc gaa gaa gct ttc gac ctc tgg aac gaa tgc gcc aaa gcc tgc gtg	48
Ala Glu Glu Ala Phe Asp Leu Trp Asn Glu Cys Ala Lys Ala Cys Val	
1 5 10 15	

ctc gac ctc aag gac ggc gtg cgt tcc agc cgc atg agc gtc gac ccg	96
Leu Asp Leu Lys Asp Gly Val Arg Ser Ser Arg Met Ser Val Asp Pro	
20 25 30	

gcc atc gcc gac acc aac ggc cag ggc gtg ctg cac tac tcc atg gtc	144
Ala Ile Ala Asp Thr Asn Gly Gln Gly Val Leu His Tyr Ser Met Val	
35 40 45	

ctg gag ggc ggc aac gac gcg ctc aag ctg gcc atc gac aac gcc ctc	192
Leu Glu Gly Gly Asn Asp Ala Leu Lys Leu Ala Ile Asp Asn Ala Leu	
50 55 60	

agc atc acc agc gac ggc ctg acc atc cgc ctc gaa ggc ggc gtc gag	240
Ser Ile Thr Ser Asp Gly Leu Thr Ile Arg Leu Glu Gly Gly Val Glu	
65 70 75 80	

ccg aac aag ccg gtg cgc tac agc tac acg cgc cag gcg cgc ggc agt	288
Pro Asn Lys Pro Val Arg Tyr Ser Tyr Thr Arg Gln Ala Arg Gly Ser	
85 90 95	
tgg tcg ctg aac tgg ctg gta ccg atc ggc cac gag aag ccc tcg aac	336
Trp Ser Leu Asn Trp Leu Val Pro Ile Gly His Glu Lys Pro Ser Asn	
100 105 110	
atc aag gtg ttc atc cac gaa ctg aac gcc ggc aac cag ctc agc cac	384
Ile Lys Val Phe Ile His Glu Leu Asn Ala Gly Asn Gln Leu Ser His	
115 120 125	
atg tcg ccg atc tac acc atc gag atg ggc gac gag ttg ctg gcg aag	432
Met Ser Pro Ile Tyr Thr Ile Glu Met Gly Asp Glu Leu Leu Ala Lys	
130 135 140	
ctg gcg cgc gat gcc acc ttc ttc gtc agg gcg cac gag agc aac gag	480
Leu Ala Arg Asp Ala Thr Phe Phe Val Arg Ala His Glu Ser Asn Glu	
145 150 155 160	
atg cag ccg acg ctc gcc atc agc cat gcc ggg gtc agc gtg gtc atg	528
Met Gln Pro Thr Leu Ala Ile Ser His Ala Gly Val Ser Val Val Met	
165 170 175	
gcc cag acc cag ccg cgc cgg gaa aag cgc tgg agc gaa tgg gcc agc	576
Ala Gln Thr Gln Pro Arg Arg Glu Lys Arg Trp Ser Glu Trp Ala Ser	
180 185 190	
ggc aag gtg ttg tgc ctg ctc gac ccg ctg gac ggg gtc tac aac tac	624
Gly Lys Val Leu Cys Leu Leu Asp Pro Leu Asp Gly Val Tyr Asn Tyr	
195 200 205	
ctc gcc cag caa cgc tgc aac ctc gac gat acc tgg gaa ggc aag atc	672
Leu Ala Gln Gln Arg Cys Asn Leu Asp Asp Thr Trp Glu Gly Lys Ile	
210 215 220	
tac cgg gtg ctc gcc ggc aac ccg gcg aag cat gac ctg gac atc aaa	720
Tyr Arg Val Leu Ala Gly Asn Pro Ala Lys His Asp Leu Asp Ile Lys	
225 230 235 240	
ccc acg gtc atc agt cat cgc ctg cac ttt ccc gag ggc ggc agc ctg	768
Pro Thr Val Ile Ser His Arg Leu His Phe Pro Glu Gly Gly Ser Leu	
245 250 255	
gcc gcg ctg acc gcg cac cag gct tgc cac ctg ccg ctg gag act ttc	816
Ala Ala Leu Thr Ala His Gln Ala Cys His Leu Pro Leu Glu Thr Phe	
260 265 270	
acc cgt cat cgc cag ccg cgc ggc tgg gaa caa ctg gag cag tgc ggc	864
Thr Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly	
275 280 285	
tat ccg gtg cag cgg ctg gtc gcc ctc tac ctg gcg gcg cgg ctg tcg	912
Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser	
290 295 300	
tgg aac cag gtc gac cag gtg atc cgc aac gcc ctg gcc agc ccc ggc	960
Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu Ala Ser Pro Gly	
305 310 315 320	

agc ggc ggc gac ctg ggc gaa gcg atc cgc gag cag ccg gag cag gcc	1008
Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln Pro Glu Gln Ala	
325 330 335	
cggt ctg gcc ctg acc ctg gcc gcc gcc gag agc gag cgc ttc gtc cgg	1056
Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu Arg Phe Val Arg	
340 345 350	
cag ggc acc ggc aac gac gag gcc gcc gcg gcc aac gcc gac gtg gtg	1104
Gln Gly Thr Gly Asn Asp Glu Ala Gly Ala Ala Asn Ala Asp Val Val	
355 360 365	
agc ctg acc tgc ccg gtc gcc gcc ggt gaa tgc gcg gcc ccg gcg gac	1152
Ser Leu Thr Cys Pro Val Ala Ala Gly Glu Cys Ala Gly Pro Ala Asp	
370 375 380	
agc ggc gac gcc ctg ctg gag cgc aac tat ccc act gcc gcg gag ttc	1200
Ser Gly Asp Ala Leu Leu Glu Arg Asn Tyr Pro Thr Gly Ala Glu Phe	
385 390 395 400	
ctc gcc gac gcc gcc gac gtc agc ttc agc acc cgc gcc acg cag aac	1248
Leu Gly Asp Gly Gly Asp Val Ser Phe Ser Thr Arg Gly Thr Gln Asn	
405 410 415	
tgg acg gtg gag cgg ctg ctc cag gcg cac cgc caa ctg gag gag cgc	1296
Trp Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu Glu Arg	
420 425 430	
ggc tat gtg ttc gtc gcc tac cac gcc acc ttc ctc gaa gcg gcg caa	1344
Gly Tyr Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala Ala Gln	
435 440 445	
agc atc gtc ttc gcc ggg gtg cgc gcg cgc agc cag gac ctc gac gcg	1392
Ser Ile Val Phe Gly Gly Val Arg Ala Arg Ser Gln Asp Leu Asp Ala	
450 455 460	
atc tgg cgc ggt ttc tat atc gcc gcc gat ccg gcg ctg gcc tac gcc	1440
Ile Trp Arg Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly	
465 470 475 480	
tac gcc cag gac cag gaa ccc gac gca cgc gcc cgg atc cgc aac ggt	1488
Tyr Ala Gln Asp Gln Glu Pro Asp Ala Arg Gly Arg Ile Arg Asn Gly	
485 490 495	
gcc ctg ctg cgg gtc tat gtg ccg cgc tcg agc ctg ccg gcc ttc tac	1536
Ala Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly Phe Tyr	
500 505 510	
cgcc acc agc ctg acc ctg gcc gcg ccg gag gcg gcg gcc gag gtc gaa	1584
Arg Thr Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu Val Glu	
515 520 525	
cggt ctg atc gcc cat ccg ctg ccg ctg cgc ctg gac gcc atc acc gcc	1632
Arg Leu Ile Gly His Pro Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly	
530 535 540	
ccc gag gag gaa gcc ggg cgc ctg gag acc att ctc gcc tgg ccg ctg	1680
Pro Glu Glu Glu Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu	
545 550 555 560	

gcc gag cgc acc gtg gtg att ccc tcg gcg atc ccc acc gac ccg cgc 1728  
Ala Glu Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr Asp Pro Arg  
565 570 575

aac gtc ggc ggc gac ctc gac ccg tcc agc atc ccc gac aag gaa cag 1776  
Asn Val Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Lys Glu Gln  
580 585 590

gcg atc agc gcc ctg ccg gac tac gcc agc cag ccc ggc aaa ccg ccg 1824  
Ala Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro  
595 600 605

cgc gag gac ctg aag 1839  
 Arg Glu Asp Leu Lys  
 610

 $\langle 210 \rangle$  2

<211> 613

<212> PRT

<213> Pseudomonas aeruginosa

<220>

<223> exotoxin A

<400> 2

Ala Glu Glu Ala Phe Asp Leu Trp Asn Glu Cys Ala Lys Ala Cys Val  
1 5 10 15

Leu Asp Leu Lys Asp Gly Val Arg Ser Ser Arg Met Ser Val Asp Pro  
20 25 30

Ala Ile Ala Asp Thr Asn Gly Gln Gly Val Leu His Tyr Ser Met Val  
35 40 45

Leu Glu Gly Gly Asn Asp Ala Leu Lys Leu Ala Ile Asp Asn Ala Leu  
50 55 60

Ser Ile Thr Ser Asp Gly Leu Thr Ile Arg Leu Glu Gly Gly Val Glu  
65 70 75 80

Pro Asn Lys Pro Val Arg Tyr Ser Tyr Thr Arg Gln Ala Arg Gly Ser  
85 90 95

Trp Ser Leu Asn Trp Leu Val Pro Ile Gly His Glu Lys Pro Ser Asn  
100 105 110

Ile Lys Val Phe Ile His Glu Leu Asn Ala Gly Asn Gln Leu Ser His  
115 120 125

Met Ser Pro Ile Tyr Thr Ile Glu Met Gly Asp Glu Leu Leu Ala Lys  
130 135 140

Leu Ala Arg Asp Ala Thr Phe Phe Val Arg Ala His Glu Ser Asn Glu  
145 150 155 160

Met Gln Pro Thr Leu Ala Ile Ser His Ala Gly Val Ser Val Val Met  
165 170 175

Ala Gln Thr Gln Pro Arg Arg Glu Lys Arg Trp Ser Glu Trp Ala Ser  
180 185 190

Gly Lys Val Leu Cys Leu Leu Asp Pro Leu Asp Gly Val Tyr Asn Tyr  
 195 200 205  
 Leu Ala Gln Gln Arg Cys Asn Leu Asp Asp Thr Trp Glu Gly Lys Ile  
 210 215 220  
 Tyr Arg Val Leu Ala Gly Asn Pro Ala Lys His Asp Leu Asp Ile Lys  
 225 230 235 240  
 Pro Thr Val Ile Ser His Arg Leu His Phe Pro Glu Gly Gly Ser Leu  
 245 250 255  
 Ala Ala Leu Thr Ala His Gln Ala Cys His Leu Pro Leu Glu Thr Phe  
 260 265 270  
 Thr Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly  
 275 280 285  
 Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser  
 290 295 300  
 Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu Ala Ser Pro Gly  
 305 310 315 320  
 Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln Pro Glu Gln Ala  
 325 330 335  
 Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu Arg Phe Val Arg  
 340 345 350  
 Gln Gly Thr Gly Asn Asp Glu Ala Gly Ala Ala Asn Ala Asp Val Val  
 355 360 365  
 Ser Leu Thr Cys Pro Val Ala Ala Gly Glu Cys Ala Gly Pro Ala Asp  
 370 375 380  
 Ser Gly Asp Ala Leu Leu Glu Arg Asn Tyr Pro Thr Gly Ala Glu Phe  
 385 390 395 400  
 Leu Gly Asp Gly Gly Asp Val Ser Phe Ser Thr Arg Gly Thr Gln Asn  
 405 410 415  
 Trp Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu Glu Arg  
 420 425 430  
 Gly Tyr Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala Ala Gln  
 435 440 445  
 Ser Ile Val Phe Gly Gly Val Arg Ala Arg Ser Gln Asp Leu Asp Ala  
 450 455 460  
 Ile Trp Arg Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly  
 465 470 475 480  
 Tyr Ala Gln Asp Gln Glu Pro Asp Ala Arg Gly Arg Ile Arg Asn Gly  
 485 490 495  
 Ala Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly Phe Tyr  
 500 505 510

Arg Thr Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu Val Glu  
           515                                  520                                  525  
 Arg Leu Ile Gly His Pro Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly  
           530                                  535                                  540  
 Pro Glu Glu Glu Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu  
           545                                  550                                  555                                  560  
 Ala Glu Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr Asp Pro Arg  
                                   565                                  570                                  575  
 Asn Val Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Lys Glu Gln  
                                   580                                  585                                  590  
 Ala Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro  
                                   595                                  600                                  605  
 Arg Glu Asp Leu Lys  
           610

<210> 3  
 <211> 35  
 <212> PRT  
 <213> Human immunodeficiency virus type 1

<220>  
 <221> PEPTIDE  
 <222> (1)..(35)  
 <223> V3 loop of MN strain of HIV-1

<400> 3  
 Cys Thr Arg Pro Asn Tyr Asn Lys Arg Lys Arg Ile His Ile Gly Pro  
       1                                  5                                  10                                  15  
 Gly Arg Ala Phe Tyr Thr Thr Lys Asn Ile Ile Gly Thr Ile Arg Gln  
                                   20                                  25                                  30  
 Ala His Cys  
           35

<210> 4  
 <211> 35  
 <212> PRT  
 <213> Human immunodeficiency virus type 1

<220>  
 <221> PEPTIDE  
 <222> (1)..(35)  
 <223> V3 loop of Thai-E strain of HIV-1

<400> 4  
 Cys Thr Arg Pro Ser Asn Asn Thr Arg Thr Ser Ile Thr Ile Gly Pro  
       1                                  5                                  10                                  15

Gly Gln Val Phe Tyr Arg Thr Gly Asp Ile Ile Gly Asp Ile Arg Lys  
                   20                  25                  30

Ala Tyr Cys  
                   35

<210> 5  
 <211> 90  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: coding strand  
           of duplex containing novel PstI site

<400> 5  
 tggccctgac cctggccgcc gccgagagcg agcgcttcgt ccggcagggc accggcaacg 60  
 acgaggcccg cgcggaacac ctgcagggcc 90

<210> 6  
 <211> 24  
 <212> PRT  
 <213> Pseudomonas aeruginosa

<220>  
 <221> PEPTIDE  
 <222> (1)..(24)  
 <223> Ib loop region of wild-type Pseudomonas exotoxin A

<400> 6  
 Gly Ala Ala Asn Ala Asp Val Val Ser Leu Thr Cys Pro Val Ala Ala  
   1                  5                  10                  15

Gly Glu Cys Ala Gly Pro Ala Asp  
                   20

<210> 7  
 <211> 28  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Ib loop region  
           of ntPE-V3MN14

<400> 7  
 Gly Ala Ala Asn Leu His Cys Gly Ile His Ile Gly Pro Gly Arg Ala  
   1                  5                  10                  15

Phe Tyr Thr Thr Lys Cys Met Gln Gly Pro Ala Asp  
                   20                  25

<210> 8  
 <211> 40  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Ib loop region  
of ntPE-V3MN26

<400> 8

Gly Ala Ala Asn Leu His Cys Asn Tyr Asn Lys Arg Lys Arg Ile His  
1 5 10 15

Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Lys Asn Ile Ile Gly Thr  
20 25 30

Ile Cys Met Gln Gly Pro Ala Asp  
35 40

<210> 9

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Ib loop region  
of ntPE-V3Th-E26

<400> 9

Gly Ala Ala Asn Leu His Cys Ser Asn Asn Thr Arg Thr Ser Ile Thr  
1 5 10 15

Ile Gly Pro Gly Gln Val Phe Tyr Arg Thr Gly Asp Ile Ile Gly Asp  
20 25 30

Asp Ile Cys Met Gln Gly Pro Ala Asp  
35 40

<210> 10

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Ib loop region  
of ntPE-fp16

<400> 10

Gly Ala Ala Asn Leu Gln Cys Arg Leu Glu Glu Lys Lys Gly Asn Tyr  
1 5 10 15

Val Val Thr Asp His Arg Leu Cys Leu Gln Gly Pro Ala Asp  
20 25 30

<210> 11

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:endoplasmic  
reticulum (ER) retention sequence



<400> 11  
Arg Glu Asp Leu Lys  
1 5

<210> 12  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: endoplasmic  
reticulum (ER) retention sequence

<400> 12  
Arg Glu Asp Leu  
1

<210> 13  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: endoplasmic  
reticulum (ER) retention sequence

<400> 13  
Lys Asp Glu Leu  
1